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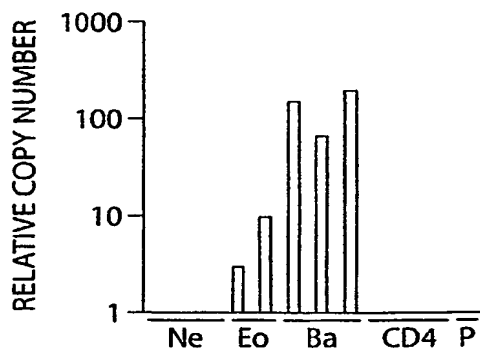


Fig. 1A

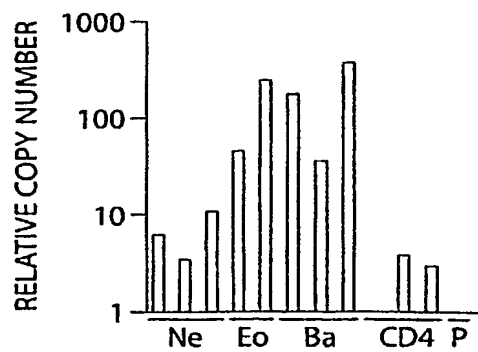


Fig. 1B

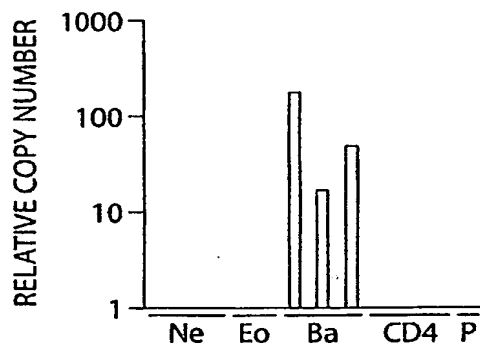


Fig. 1C

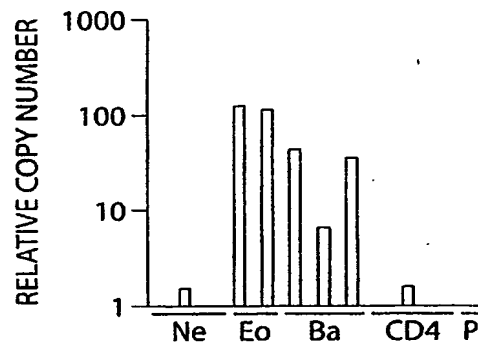


Fig. 1D

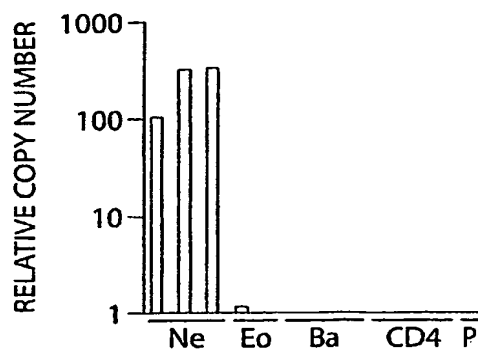


Fig. 1E

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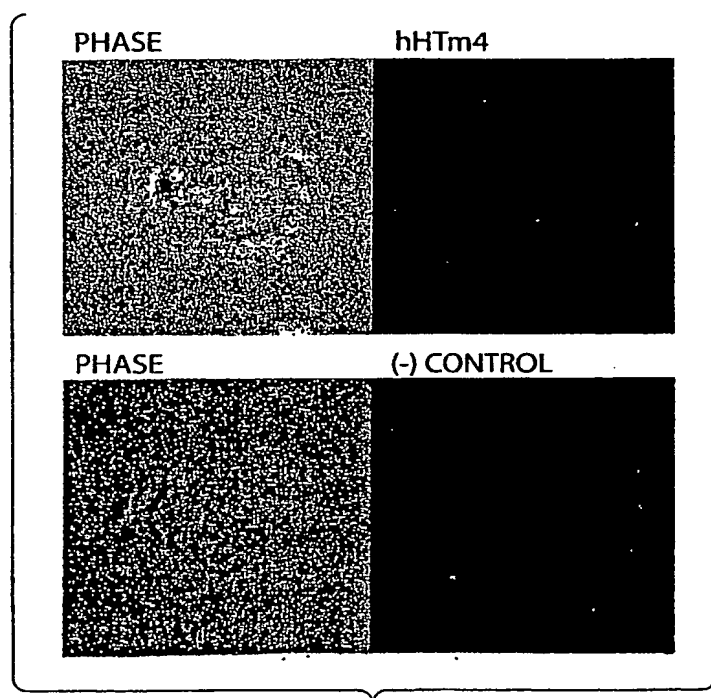


Fig. 2

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Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

Ion Channels		Cell-type ^a	MC	Ba	Eo	Ne	Pl	CD4	CD8	CD14	CD19	Fb	TC ^b	Gene Functions
Transcript (Accession #, GenBank)														
<u>Ca²⁺ channel type A1 D (BE550599)</u>		Ba, Eo	0.1	1.7	1.5	0.4	0.0	0.3	0.1	0.0	0.3	0.0	0	facilitates uptake of the metalloids arsenite and antimonite
<u>aquaporin 9 (NM_020980) 602914</u>		Ne	0.7	0.1	0.4	137.4	0.4	0.9	0.1	8.6	0.1	0.2	7	
<u>K⁺ channel Kir 1.3 (U73191) 600359</u>		Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>K⁺ channel Kir 2.1 (AF153820) 600681</u>		Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>GPCR</u>														
<u>histamine H₄ R (AF312230) 606792</u>		Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u>PGE⁺ R type 3a2 (X83858) 176806</u>		Ba	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	0	signaling pathways
<u>C3a R (U62027) 605246</u>		Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	3	anaphylatoxin receptor
<u>CCR3 (NM_001837) 601268</u>		Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	0	importance for eosinophil responses
<u>CRTH2 (NM_004778) 604837</u>		Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u>EMR-1 (NM_001974) 600493</u>		Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	Probably involved in cellular response to a hormone
<u>adenosine A₃ R (NM_000677) 600445</u>		Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	0	cardioprotective function
<u>P2Y2 purinergic R (NM_002564) 600041</u>		Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	0	P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
<u>GPR 105 purinergic R (NM_014879)</u>		Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	2	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
<u>GPR, Edg-4 (AF011466) 605110</u>		Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	edg-4 min was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant
<u>PAR1-like GPR43 (NM_005306)</u>		Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	the highest levels of gpr43 were

Fig. 3A

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Fig. 3C

Fig. 3C

VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL- CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of fMLF CSL2 is an anaphylatoxin- binding protein with unique ligand binding and signaling properties GPR86 proved to be a G(i)- coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13) PAR2 plays a key role in chronic joint inflammation responsible for initiating the allergic response Cell cycle regulator promotes the proliferation and differentiation of hematopoietic cells engagement of 2B4 with specific antibody activates NK cytolytic activity Receptor for acidic and basic fibroblast growth factors. lacking either 115ra or Sox4 have defects in B-cell development SIGLEC8 expression on eosinophils but not other leukocytes Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro OBSP1 is almost exclusively expressed on B cells. MS4A2 Allergic disease receptor-mediated endocytosis												
formyl peptide R 2 (<u>U81501</u>)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	5
GPR77 (<u>NM_018485</u>)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	2
GPR86 purinergic R (<u>NM_023914</u>)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	1
PAR2 (<u>BE965369</u>) <u>600933</u>	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	15
<i>Other Receptors</i>												
Fc ε RI α (<u>BC005912</u>) <u>147138</u>	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	0
<u>HTM4</u> (<u>L35848</u>) <u>606498</u>	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	1
IL-3 R (<u>NM_002183</u>) <u>308385</u>	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	0
CD244 NK cell R <u>NM_016382</u> <u>605554</u>	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	0
fibroblast growth factor R 2 (<u>NM_022969</u>) <u>176943</u>	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	17
IL-5R α (<u>M75914</u>) <u>147851</u>	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	0
Siglec 8 (<u>NM_014442</u>) <u>605639</u>	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	0
CD117 c-KIT (<u>NM_000222</u>) <u>164920</u>	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	15
Sigtec8 D86358 <u>604405</u>	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	0
Fc ε RIβ (<u>NM_000139</u>) <u>147138</u> low density lipoprotein R	MC, Ba MC, Ba	22.3 20.7	44.3 20.4	0.4 1.3	0.6 1.8	1.6 2.3	0.5 2.1	0.2 3.4	0.0 3.5	0.3 0.8	0.1 6.3	0 34

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(NM_000527) 606945 TRK neurotrophin R (NM_002529) 191315	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes
butyrophilin like R (AK025267)	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	1	1	his gene is mainly expressed in small intestine, colon, testis, and leukocytes
CD120a, TNF-R-1 (NM_001065) 191190	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35	35	Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.
CD95, Fas, APO-1 (AA164751) 134637	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	7	7	Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted

Fig. 3D

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isoforms 2 to 6 block apoptosis
(in vitro).

does not induce apoptosis.

decoy R1, TRAILR3 (AF012536) 603613	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	0
FcγR IIc2 (U90939)	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	2
FcγR IIc3 (U90940)	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	5
FcγR III (J04162) 146740	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	4
G-CSF R (NM_0007601) 138971	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	3
IL-13 R (U81379) 308385	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	0
IL-1R, type II (NM_004633) 147811	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	3
IGFR 1 (NM_000875) 147370	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	3
IGFR 2 (NM_000876) 147280	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	32
leukocyte immunoglobulin-like R A2 (NM_006866) 604812	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	2
Toll-like R 1 (AL050262) 601194	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	0
Toll-like R 2 (NM_003264) 603028	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	0
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	0

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4⁺ cells (CD4), CD8⁺ cells (CD8), CD14⁺ cells (CD14), CD19⁺ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

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	CB cultured		cultured		Eosinophils		Neutrophils		platelets		Erythrocytes		CD4		CD8		CD14		CD19	
	MCs	Basophils	basophils	basophils																
Spink5	21	17	11	22	16	30	15	28	36	129	104									
chymase human	1221	47	65	45	12	101	62	108	59	104	45									
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39									
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6									
tryptase delta	349	45	6	23	55	74	113	11	10	42	11									
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83									
TRPV2	129	37	15	97	99	259	137	133	67	97	110									
ANKTM1_	28	28	8	38	30	96	18	14	46	11	28									
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54									
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421									

Fig. 4A

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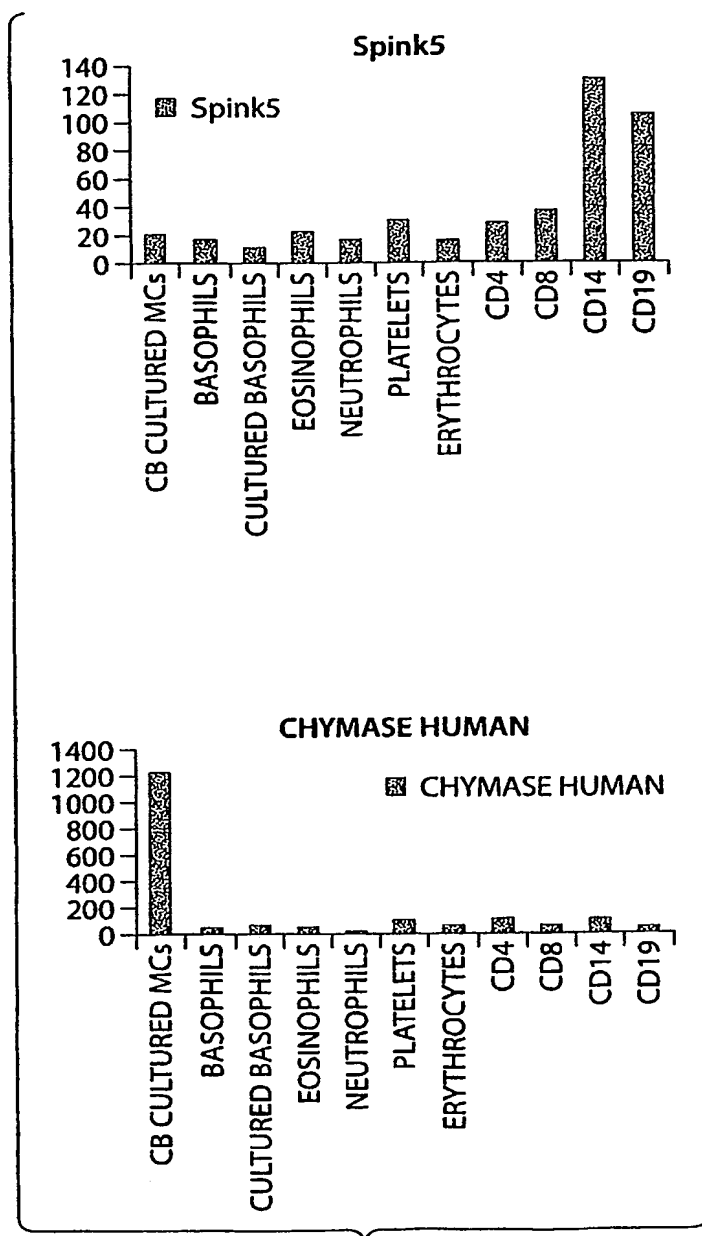


Fig. 4B

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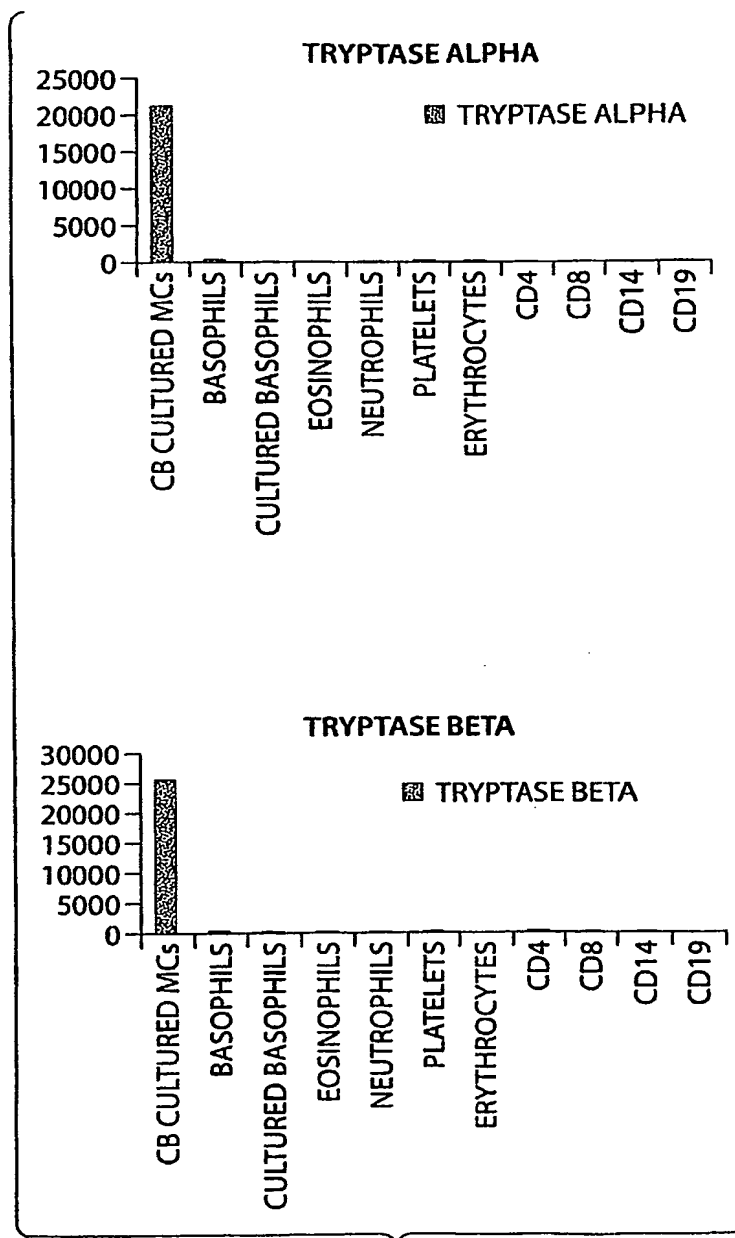


Fig. 4C

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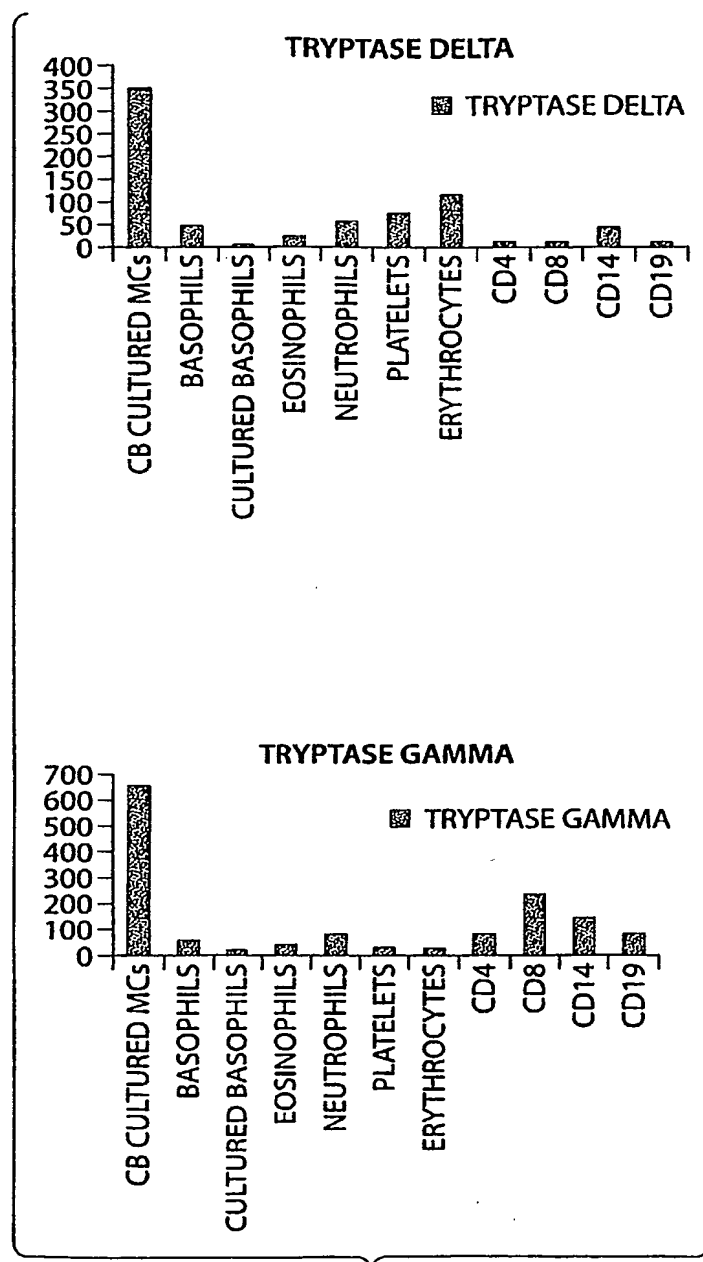


Fig. 4D

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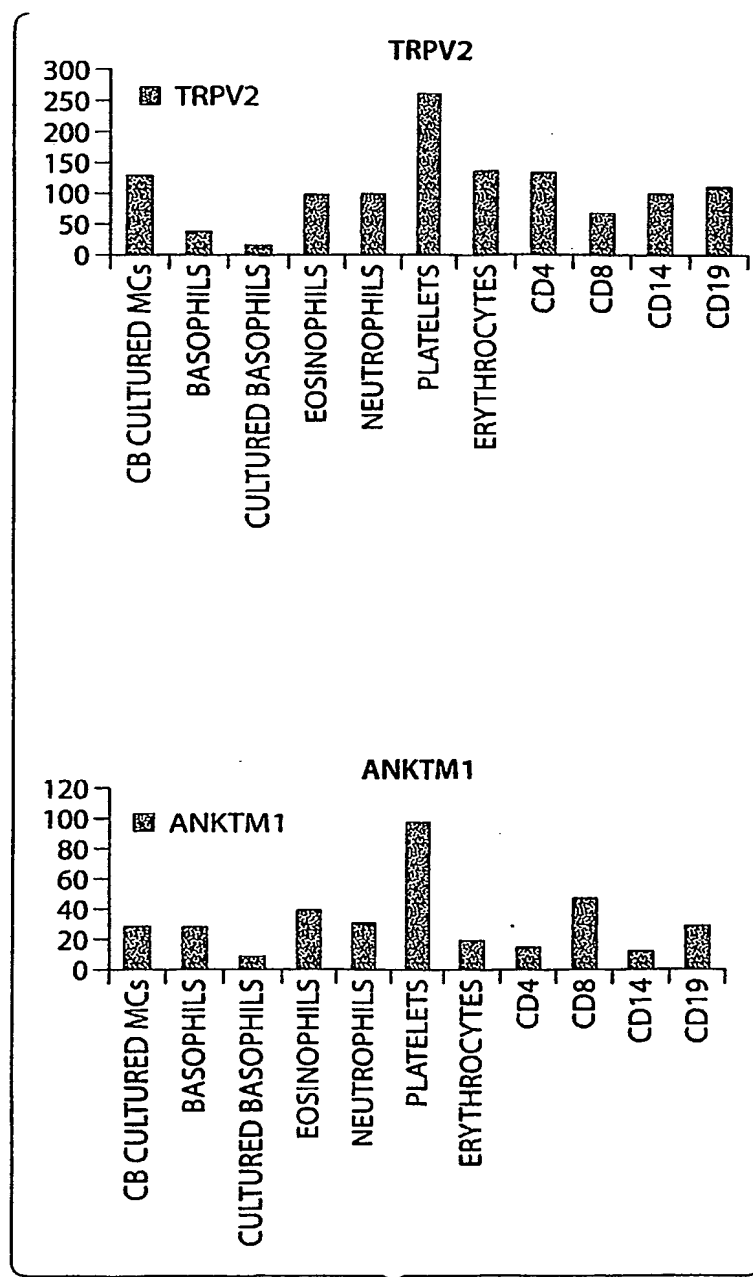


Fig. 4E

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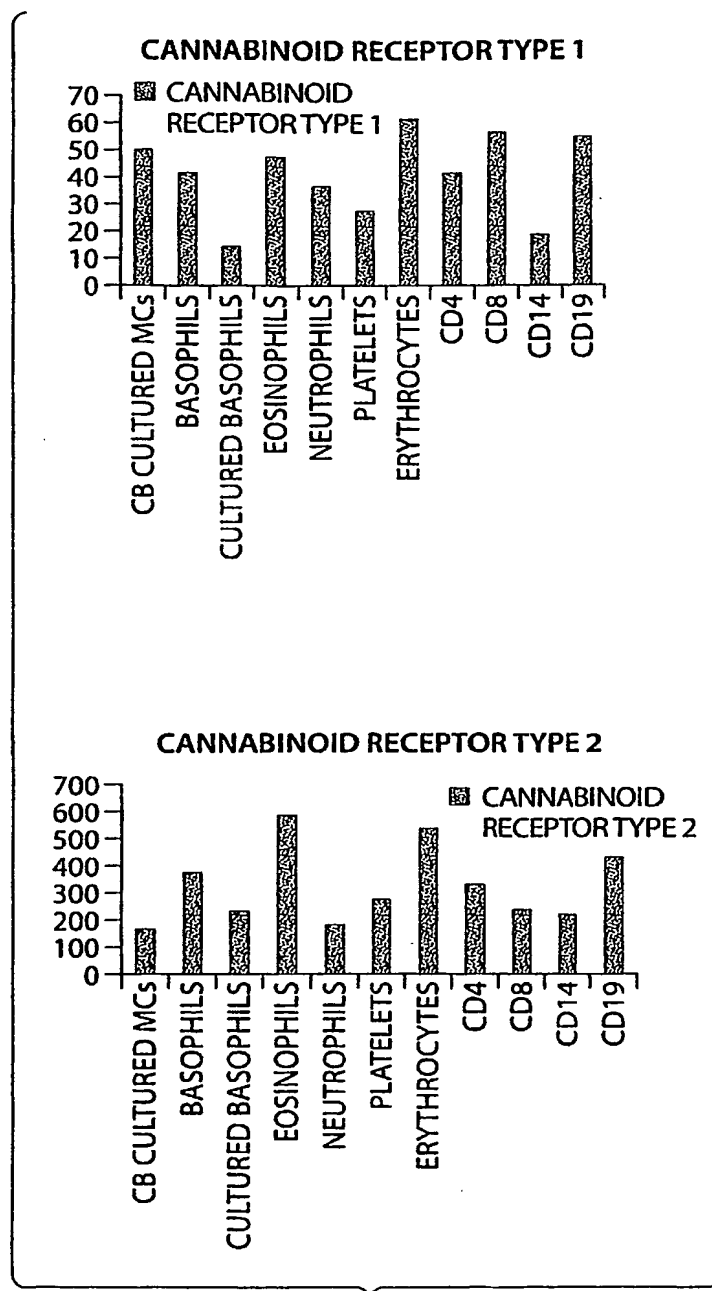


Fig. 4F

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CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
86	28	39	26	37	125	46	103	95	85	28
4	45	1004	59	84	18	68	31	68	451	13
165	84	51	258	1261	31	42	13	18	1105	125
375	780	227	1755	4237	199	375	286	58	2963	214
49	614	384	461	3269	146	318	8	9	1247	52
28	50	45	154	389	120	148	127	35	539	86
7	58	34	18	23	13	106	14	286	68	204
22	17	21	27	28	35	11	28	110	88	111
30	54	134	66	61	149	95	39	247	147	271
35	138	81	88	93	191	132	57	257	21	267
24	31	23	21	21	53	27	33	135	19	173
139	140	85	157	144	280	210	35	239	152	196
11	45	41	50	41	88	15	19	72	77	85
41	43	31	20	52	31	121	96	163	26	193
27	83	24	41	49	61	239	92	323	56	72
68	89	41	51	95	75	97	76	169	36	196
144	621	83	1334	2386	107	146	145	52	2154	99
18	14	5	28	37	86	12	13	14	32	23

Fig. 5A

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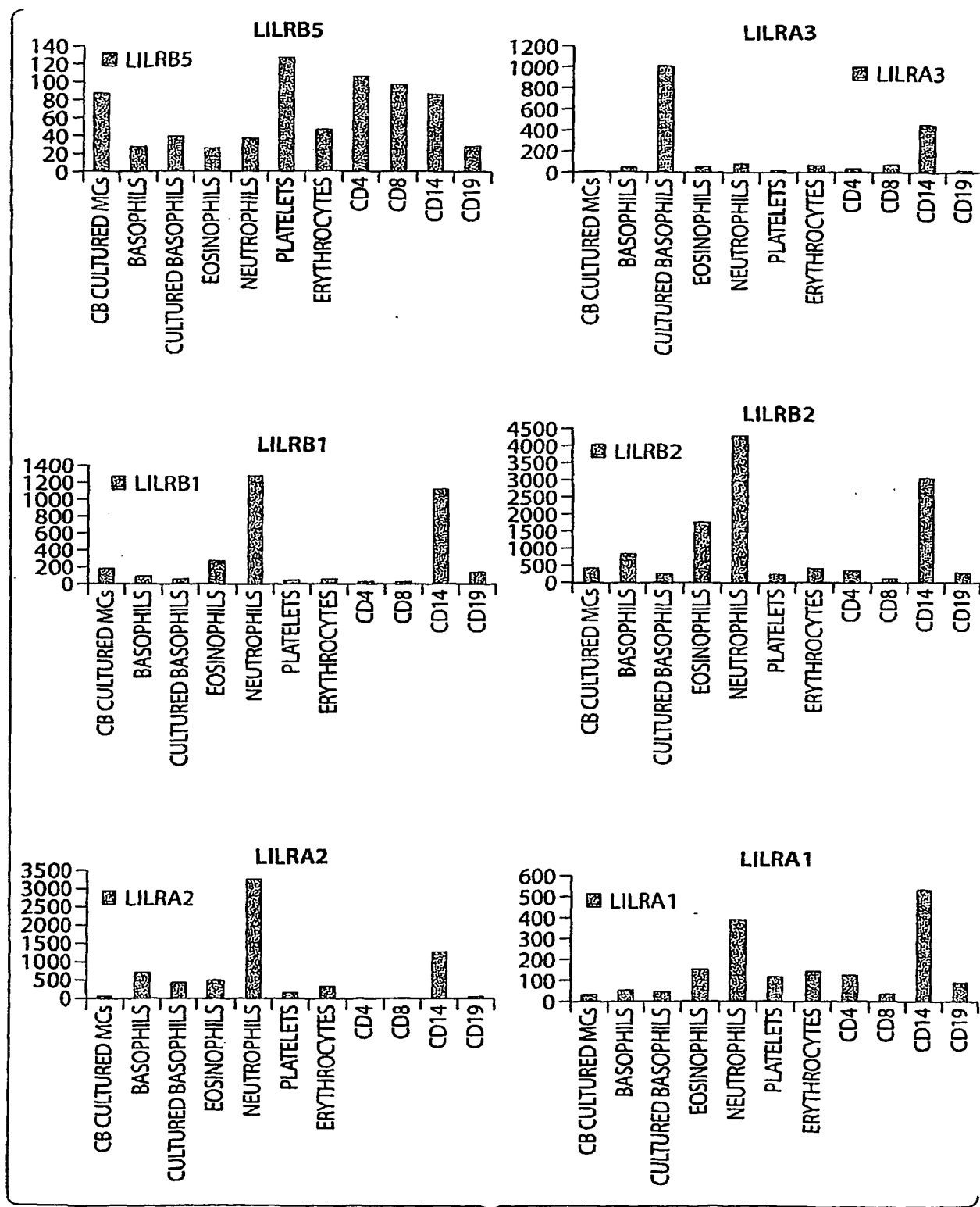


Fig. 5B

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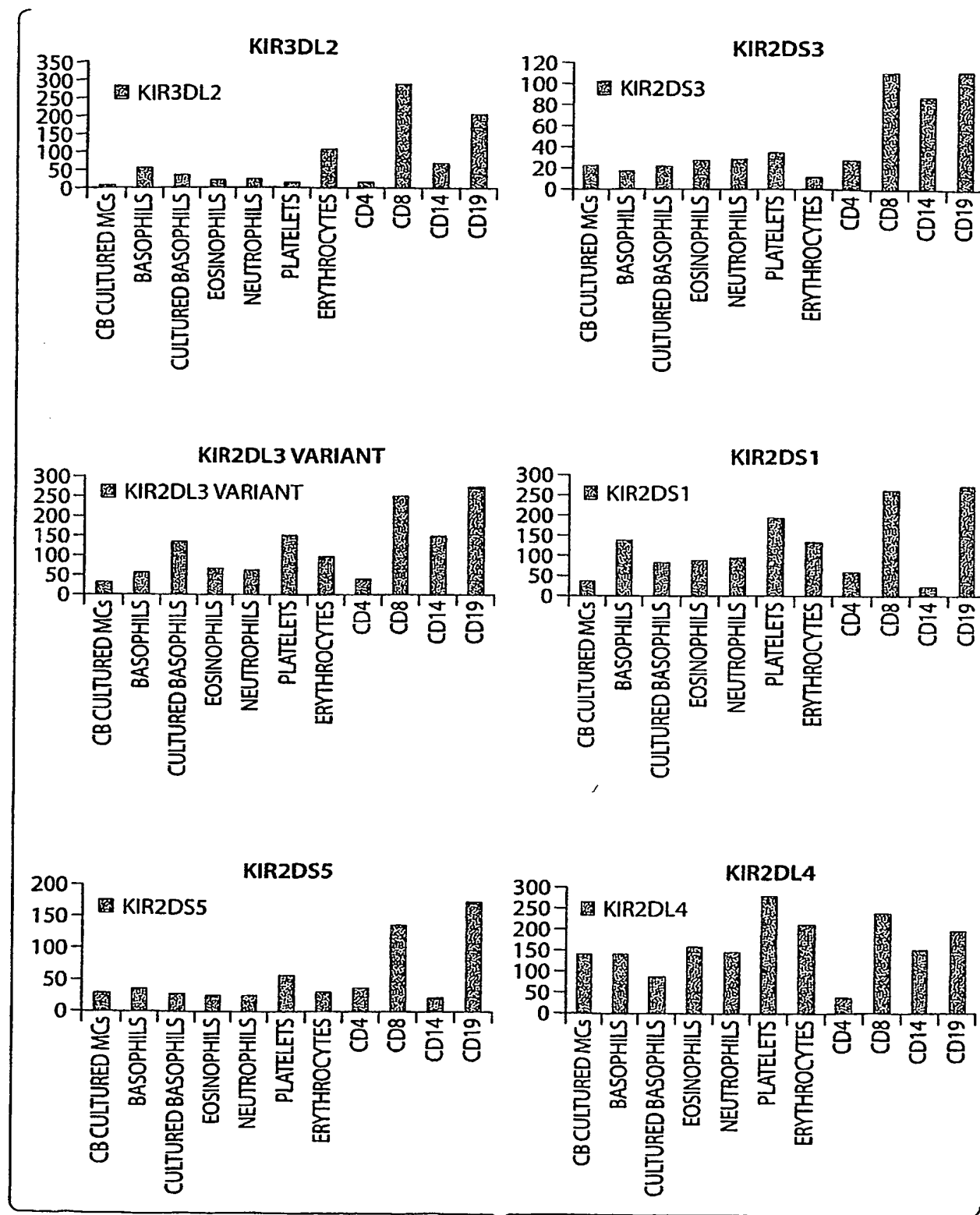


Fig. 5C

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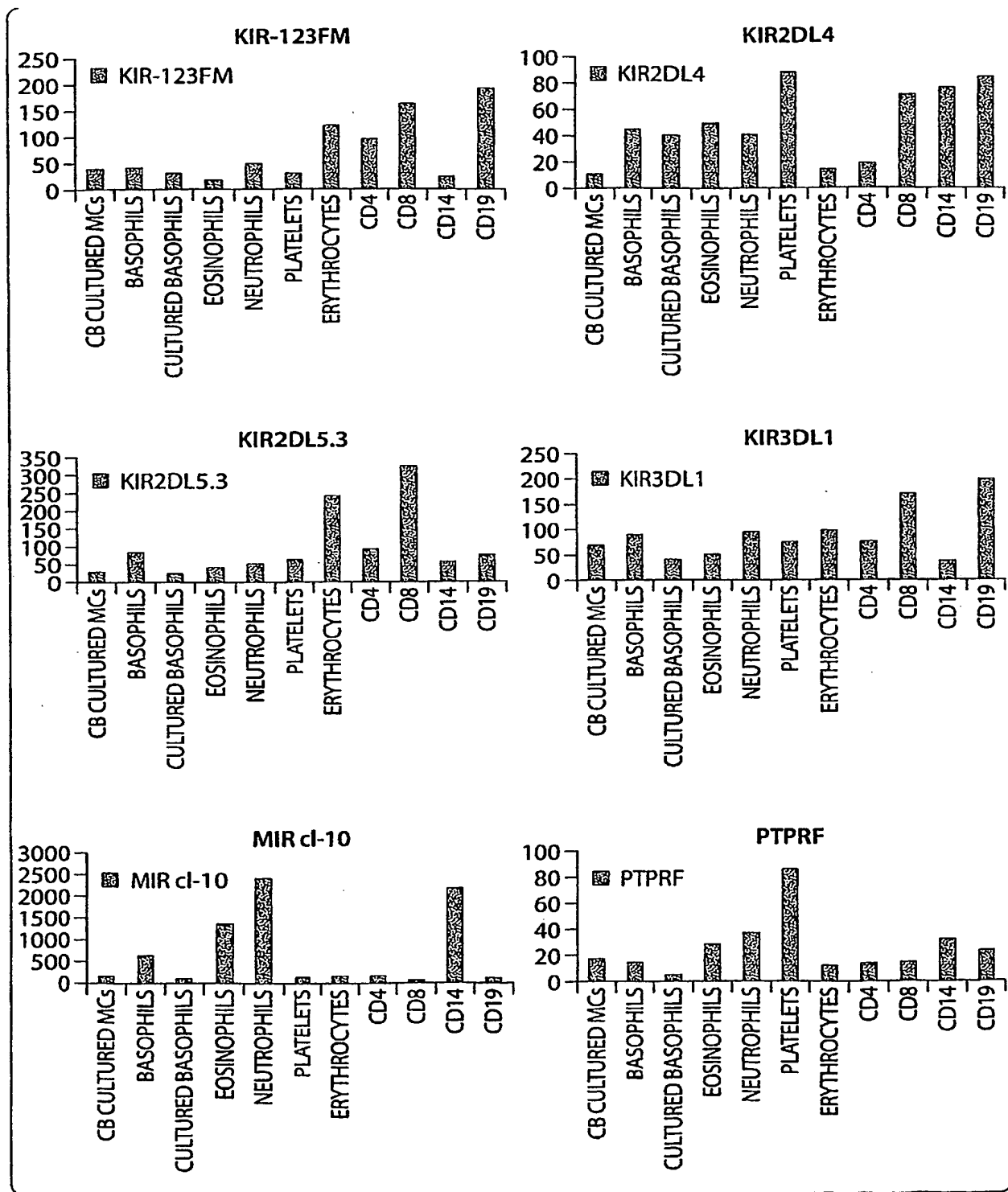


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4⁺ cells, CD8⁺ cells, CD14⁺ cells, CD19⁺ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. *Italic numerals* show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC	Ba1	Ba2	Ba3	Eo	Eo	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	pl	CD4	CD8	CD14	CD19	Fb	Ba.S.I.
207539_s_at	NM_000589.1	IL-4	0.2	0.1	10.4	16.9	13.4	0.1	0.0	0.2	0.1	0.1	0.3	0.0	1.2	0.2	0.0	0.2	0.1	0.0	0.0	73348
210254_at	L35948.1	HTrm4	0.8	0.4	115.6	130.1	153.6	2.4	1.7	21.8	1.7	0.1	0.9	3.6	9.5	0.2	0.5	0.4	0.1	0.2	0.0	3824
205513_at	NM_001062.1	vitamin B12 binding protein	1.5	1.2	98.9	149.3	110.9	3.2	2.2	16.1	1.9	4.9	4.5	6.3	8.1	1.8	0.7	0.8	1.4	0.9	0.1	20322
206148_at	NM_002183.1	IL-3 R	1.0	0.1	6.2	80.2	71.3	1.7	1.7	1.8	2.9	0.3	0.4	0.2	1.9	0.2	0.3	0.2	0.7	0.1	0.1	1662
214920_at	R33964	FLJ11022 fis	0.1	1.1	4.9	13.1	15.4	0.1	0.2	0.7	0.5	1.0	0.4	0.5	0.7	0.1	0.1	0.2	0.1	0.3	0.1	16049
201825_s_at	AL572542	CGI-49	3.3	1.6	21.4	74.9	46.5	2.1	1.2	0.1	1.2	0.1	0.1	0.2	0.1	1.3	0.7	1.7	1.4	0.8	2.8	15045
213238_at	AI478147	ATPase Class V type 10D	1.2	2.9	39.9	76.3	118.9	2.3	1.7	3.1	1.9	2.1	1.4	2.3	6.8	0.7	0.9	0.9	2.5	5.0	4.1	14398
211734_s_at	BC005912.1	Fc epsilon RI alpha	10.5	28.4	210.0	220.8	226.2	8.4	2.1	4.8	2.9	0.3	0.7	4.5	16.6	1.4	5.1	0.8	1.4	0.4	0.2	12703
213894_at	BF447246	KIAA0950	0.1	0.0	3.7	13.0	15.6	0.3	0.4	0.4	0.4	0.9	0.7	0.7	0.6	0.5	0.6	0.1	0.1	0.2	0.2	12272
206363_at	NM_005360.2	c-MAF	3.7	1.4	36.5	75.7	66.4	1.2	0.1	0.2	0.2	0.2	0.1	0.2	1.0	0.6	4.8	2.7	0.5	1.0	0.0	11927
203373_at	NM_003877.1	SOS2	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	6.5	0.7	1.2	0.3	2.5	1.6	3.2	3.5	0.8	0.9	3.6	98282
207538_at	NM_000589.1	IL-4	0.3	0.1	5.4	9.8	9.2	0.4	0.4	0.0	0.3	0.1	0.0	0.4	0.7	0.8	0.4	0.3	0.1	0.0	0.1	98156
213684_s_at	BF671400	LIM-protein	0.6	0.1	11.1	21.0	20.6	1.9	1.6	2.4	1.8	0.8	0.6	1.5	2.5	0.1	0.0	0.3	1.0	0.0	0.1	89245
209360_s_at	D43968.1	AML1b protein	10.4	2.4	53.2	131.1	90.5	8.5	7.0	13.8	11.3	0.5	0.5	0.5	4.2	1.3	4.1	5.9	1.3	2.5	3.1	87543
202034_at	NM_004056.2	carbonic anhydrase VIII	0.4	0.1	11.7	10.2	6.0	1.2	0.1	0.2	0.4	0.8	0.9	0.1	0.5	0.5	1.1	0.1	0.1	0.8	0.0	81309
210643_at	AF033712.1	osteopontin ligand	0.1	0.3	1.8	3.4	6.0	0.7	0.4	0.3	0.2	0.4	0.1	0.3	0.1	0.1	0.3	0.4	0.3	0.2	0.2	76628
209211_at	AF132818.1	colon Kruppel-like factor	0.1	0.0	1.8	10.2	8.8	0.3	0.5	1.5	0.8	1.1	0.7	0.8	0.5	0.2	0.2	0.4	0.2	0.1	0.3	7239
204309_at	NM_000781.1	CYP11A	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.1	0.9	0.3	0.3	0.1	0.0	0.3	0.7	68366
203372_s_at	AB049031	SOS2	0.6	1.6	9.2	8.5	15.9	1.4	2.4	0.9	0.2	0.7	0.6	0.4	0.8	0.8	1.6	1.3	0.3	0.3	1.4	68271
207463_x_at	NM_002771.1	serine protease 3 (trypsin 3) acid sphingomyelinase-like	1.0	1.0	4.8	10.0	10.9	0.4	1.0	1.0	1.2	1.2	0.9	1.0	1.8	0.4	0.6	0.4	0.3	0.7	1.2	67218

Fig. 6A-1

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Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo (small)	Eo3 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	BaSL
213624_at	AA873600	phosphodiesterase	4.7	2.0	20.8	30.6	25.9	2.1	2.8	1.7	0.5	1.1	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.6946
214873_at	AL137651.1	clone DKFZp434O0213	0.1	0.4	3.7	15.5	24.4	2.0	0.9	2.5	0.2	0.1	0.7	0.6	0.1	1.1	0.5	0.6	0.7	6.2585
204928_s_at	NM_019848.2	protein P3	2.3	1.5	9.8	49.0	34.3	3.7	3.3	4.8	4.2	1.6	1.0	2.2	4.1	1.8	0.8	2.0	2.6	6.2142
208935_s_at	L78132.1	prostate carcinoma tumor antigen (pcta-1)	2.2	1.2	9.9	19.1	16.6	2.3	1.5	3.6	2.5	1.1	1.1	1.9	0.9	1.8	2.0	1.4	0.8	6.2011
203201_at	NM_000303.1	phosphomannomutase 2 (PM42)	1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.1	6.1557
201826_s_at	NM_016002.1	CG-49	1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	0.6	5.6407
213421_x_at	AW007273	serine protease 4 (trypsin 4)	1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	5.4082
209348_s_at	AF05376.1	c-MAF, short form	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	0.7	0.7	1.4	5.3183
213343_s_at	AL041124	hypothetical protein PP1665	0.9	0.2	12.2	17.0	12.0	3.5	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	5.2721
202491_s_at	NM_003640.1	kappa B-associated protein	1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	5.107
221021_s_at	NM_030877.1	Bos taurus P14 protein	6.9	3.2	7.2	29.2	58.9	2.8	3.2	5.4	6.3	0.9	1.2	1.8	1.6	1.6	2.2	2.4	2.0	4.9129
213346_at	BE748563	hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	4.0	6.7	6.2	4.8	1.4	0.9	0.8	1.1	0.2	1.2	1.5	0.6	4.8879
209764_at	AL022312	mannosyl (beta-1,4)-glycoprotein	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.4	4.855
207067_s_at	NM_002112.1	beta-1,4-N-acetylglucosaminyltransferase	64.1	14.7	105.2	164.9	165.7	3.4	1.4	4.1	2.8	2.1	1.2	4.6	14.0	2.4	0.8	0.9	1.1	4.6305
210375_at	X83858.1	histidine decarboxylase	1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	4.6103
206306_at	NM_001036.1	prostaglandin E receptor, type 3a2	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	4.5552
210001_s_at	AB005043.1	ryanodine receptor 3 (RyR3)	5.2	0.2	3.0	24.1	29.9	2.1	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.9	4.5248
		SOC51																		
		serine (or cysteine) proteinase inhibitor, class B (ovalbumin), member 2																		
204614_at	NM_002575.1	(SERPINB2)	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	0.2	4.5061
209960_at	X16323.1	hepatocyte growth factor (HGF)	0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	0.5	4.4335
209212_s_at	AB030824.1	transcription factor BTEB2	0.1	0.2	7.5	14.3	22.1	2.3	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	0.8	4.363

Fig. 6A-2

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC	MC lung	Ba1	Ba2	Ba3	EO	EO	EO3	EO4	Ne	Ne2	Ne3	Ne4	CD4	CD8	CD14	CD19	Fb	Ba.S.
214651_s_at	U41813.1	class 1 homeoprotein (HOXA9)	0.6	0.6	1.7	6.3	8.3	0.3	0.5	0.8	0.5	0.1	0.1	0.5	1.0	1.0	0.1	0.3	0.1	0.1	4.3618
35502_at	AL041124	DNFZP434D0316_s1	1.6	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	2.5	2.3	1.8	4.3594
205373_at	NM_004389.1	catenin (cadherin-associated protein) alpha 2	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.7	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.2	0.2	4.2308
219676_at	NM_025231.1	FLJ22191	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	0.2	2.2	0.6	1.1	1.4	0.3	0.1	4.2135
213385_at	AK026415.1	beta2-microglobulin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	1.0	0.2	1.5	0.8	1.0	0.1	0.9	1.6	0.3	0.2	4.2131
214637_at	BC437034	oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.1	0.0	4.1983
202490_at	AF153419.2	keap1-associated protein	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.3	0.0	0.2	0.0	0.3	0.3	0.5	0.2	0.4	4.1747
220416_at	NM_024837.1	FLJ21472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	4.1718
218318_s_at	NM_016231.1	nemo-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	0.1	1.6	1.3	0.9	1.2	1.1	4.1558
215201_at	AW166925	FLJ14135 fcs clone MAMMA1002728	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.1	0.5	0.3	0.8	0.4	0.5	4.1491
222303_at	AV700891	ETS2 intronic transcript 1 mRNA	0.6	1.4	3.1	8.68	63.8	3.6	2.2	2.9	3.2	10.8	10.5	16.6	19.0	12	0.7	0.7	8.1	0.3	4.0555
201664_at	AL136877.1	DNFZP434F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	3.8471
210252_s_at	AB002356.1	MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	3.8424
201328_at	AL575509	vets avian erythroblastosis virus E26 oncogene homolog 2	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	3.8075
218392_x_at	NM_022754	FLJ12876	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	3.7603
205046_at	NM_011813.1	FLJ14150 fcs clone MAMMA1003026	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	3.7324
211770_at	AF122301.1	histamine H4 receptor	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	3.6719
201663_s_at	NM_005496.1	chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	3.6472
208933_s_at	AL659005	lectin, galactoside-binding, soluble, 8 (galactin 8)	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	3.6311
209710_at	AL563460	GATA-binding protein 2	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	3.6251
205769_at	NM_003645.1	fatty acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.3	3.5389
209409_at	D86962.1	KIAA0207	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.7	1.5	0.4	3.4907
38388_at	AB002356	KIAA0358	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	3.4534
205899_at	NM_003914.1	cyclin A1	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.3	3.3824
218150_at	NM_012097.1	ADP-ribosylation factor-like 5	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	3.3745
213097_s_at	AL338837	zuculin related factor 1	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	3.3	3.3672
208158_s_at	NM_018030.1	oxysterol-binding protein-related protein nasopharyngeal carcinoma associated	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	3.342
210109_at	AF191492.1	gene protein 8	12	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	3.2977
220918_at	NM_025143.1	FLJ20856	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	3.2902
209359_x_at	L34598.1	aml1 (acute myeloid leukemia 1) oncogene	12	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	1.0	0.8	0.6	3.2789
208107_s_at	NM_030941.1	exonuclease NEF-sp	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	3.2356
212412_at	AV715767	DNFZP434A072	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	3.2017
215215_s_at	AC004381	chromosome 16 BAC clone	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	3.198
221509_at	AB014731.1	SNAP-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	4.1	7.5	3.1618
218637_at	NM_018439.1	hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	1.1	3.1587
218352_at	NM_018191.1	hypothetical protein FLJ10716	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	3.1058
213035_at	AA081194	KIAA0379	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	2.2	3.0937
211180_x_at	D89788.1	aml1 (acute myeloid leukemia 1) oncogene	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	1.7	0.4	0.4	0.6	1.1	0.7	3.0936
210731_s_at	AL136105	lectin, galactoside-binding, soluble 8 (galactin 8)	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.7	1.3	3.0876
203164_at	BE464756	acetyl-Coenzyme A transporter fatty acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	3.063
205768_s_at	NM_003645.1	A kinase (PRKA) anchor protein (gravin) 12	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.1	3.0353
210517_s_at	AB003476.1	Ca2+-independent phospholipase A2 short isoform	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.3	3.0146
210647_x_at	AF102988.1		2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	3.002

Fig. 6B

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC	MC	Ba1	Ba2	Ba3	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	EsSL	
207328_at	NM_001140.1	15-lipoxygenase	0.1	0.6	0.7	0.7	0.7	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.1	74.129
219695_at	NM_024703.1	FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	19.123
208253_at	NM_014442.1	salic acid binding lg-like lectin, Siglec B	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	9.8056
211922_s_at	AV028632.1	catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125
201802_at	NM_004955.1	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989
214523_at	NM_001805.1	CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462
210079_at	M34455.1	interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078
215573_at	AU147084	FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983
201801_s_at	AF079117.1	solute carrier family 29 (nucleoside transporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314
213825_at	AF221520.1	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987
219821_s_at	NM_018988.1	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284
205472_s_at	NM_004392.1	daechurid (Drosophila) homolog KIAA0095	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088
202188_at	NM_014669.1	chemokine CCL23	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499
210548_at	U58913.1	chemokine CCL23	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082
209447_at	AF043290.1	lymphocyte membrane associated protein (887)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	2.7	5.1472
206171_at	NM_000677.2	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469
210549_s_at	U58913.1	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873
214183_s_at	X91817.1	transketolase-like protein spectrin repeat containing, nuclear envelope	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.7	0.6	0.0	4.7894
215350_at	AB033088.1	envelope	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822
206277_at	NM_002564.1	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043
204776_at	NM_003248.1	thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746
201563_at	L29008.1	L-idoal-2 dehydrogenase	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557
206637_at	NM_014879.1	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761
213622_at	A1733465	collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576
214705_at	AJ001306.1	PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532
266_s_at	L3930	CD24 signal transducer	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	4.3	0.2	3.3793
201432_at	NM_001752.1	catalase (CAT)	23.0	14.3	35.7	49.4	19.9	202.3	209.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325
209696_at	D26054.1	fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.5	1.9	2.0	1.6	8.1	1.1	0.6	3.3089
216379_x_at	AK000168.1	CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741
205569_at	NM_014398.1	lysosome-associated membrane glycoprotein (LAMP3)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308
219233_s_at	NM_018530.1	hypothetical protein PRO2521	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093
202286_s_at	J04152	gastrointestinal tumor-associated antigen GA733-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844
206442_at	NM_003007.1	semenogelin I (SEMG1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837
205733_at	NM_000057.1	Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427
204392_at	NM_003566.2	calcium/calmodulin-dependent protein kinase I (CAMKI)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763
213497_at	AL050374.1	DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099
219296_at	NM_019028.1	similar to ankyrin repeat-containing protein AKR1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018

Fig 6C

Fig. 6C

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C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC	cord blood	MC	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO1 (small)	EO2 (small)	EO3 (small)	EO4 (small)	Ne (small)	Ne3 (small)	Ne4 (small)	CD4	CD8	CD14	CD19	CD19	Ne5L
205403_at	NM_004633.1	Interleukin 1R type II		0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.4	0.1	0.2	0.0	0.0
216782_at	AK026679.1	FLJ23026 fts		0.0	0.2	0.2	0.1	0.1	0.1	0.1	0.5	0.2	33.2	31.5	17.4	0.1	0.1	0.1	0.1	0.2	0.2
210119_at	U73191.1	ICN		0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0
209395_at	M80927.1	KCNJ15 inward rectifier potassium channel Kir1.3		1.5	0.2	0.9	0.1	0.4	0.3	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.0
203691_at	NM_002638.1	chitinase 3-like 1 (cartilage glycoprotein-39)		0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5
211372_s_at	U64094.1	R		0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0
207008_at	NM_001557.1	GPR		0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	129.8	168.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6
206515_at	NM_000896.1	leukotriene B4 omega hydroxylase (CYP4F3)		0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3
204007_at	J04162.1	R		0.8	0.7	1.4	1.6	1.8	1.1	1.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6
204470_at	NM_001511.1	melanoma growth stimulating activity, alpha		1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1
206025_s_at	AW188198	tumor necrosis factor, alpha-induced protein 6		0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3
209396_s_at	M80927.1	chitinase 3-like 1 (cartilage glycoprotein-39)		1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1
211806_s_at	D87291.1	ICN		0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9
211920_s_at	B667761	R		0.4	0.8	0.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	46.8	2.5	0.7	0.3	1.8	1.1
207094_at	NM_000634.1	GPR		0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.3	62.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1
213589_s_at	AW68201	23kDa mRNA sequence		0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1
218963_s_at	NM_015515.1	DKFZP434G032		0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	46.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1
213506_at	B965369	PAR2 proteinase activated receptor-2		0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.6	0.4
220187_at	NM_024636.1	GPR		0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1
206026_s_at	NM_007115.1	FLJ23155		0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1
41469_at	L10343	tumor necrosis factor, alpha-induced protein 6		1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5
205568_at	NM_020980.2	ICN		0.5	0.9	0.1	0.1	0.1	0.3	0.1	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.5
210483_at	BC005043.1	R		0.1	0.1	0.4	0.9	0.7	1.0	0.9	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.1
215223_s_at	W46388	superoxide dismutase 2		4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2
210484_s_at	BC005043.1	R		0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4
205654_at	NM_000715.4	complement component 4-binding protein, alpha		0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2
210773_s_at	U81501.1	GPR		0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8
206222_at	NM_003841.1	R		1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5
207083_s_at	NM_003003.1	SEC14 (S. cerevisiae)-like 1		0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0
211163_s_at	AF012536.1	R		0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1
205931_s_at	NM_004904.1	decoy receptor 1, TRAILR3 cAMP response element-binding protein CRE-BPa		0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1
205922_at	NM_004665.1	R		0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7
210176_at	AL050262.1	vanin 2		0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.2	29.5	38.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5
215977_x_at	X68285.1	Toll-like receptor 1		1.9	0.9	0.8	0.7	0.3	0.3	0.6	1.0	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.3
215783_s_at	X14174.1	glycerol kinase		0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	0.6	21.2	42.8	11.6	12.8	1.2	0.7	0.2	0.5	0.5
217167_x_at	AJ252550	liver-type alkaline phosphatase		1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.3	6.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2
213349_at	A934439	GK gene for glycerol kinase exon 1 KIAA0779		0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.5	1.6	1.2

Fig. 6D

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C. Neutrophil (Ne)-selective transcripts (2/77).

Probe set	Accession #	Transcripts	MC cond blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	p1	CD4	CD8	CD14	CD19	Fb	Ne.S1	
210789_x_at	U06921	carcinoembryonic antigen (CGM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	19.4	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749
210772_at	M68107.1	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	5.6	0.1	0.1	9.2661	
218978_s_at	NM_018586.1	PRO1584	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	28.2	0.2	0.7	0.4	1.1	0.2	0.4	9.1536
204006_s_at	NM_000570.1	<i>Fe gamma R IIb (CD16)</i>	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769
207275_s_at	NM_001995.1	fatty acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855
220302_at	NM_001596.2	male germ cell-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8.866
221803_s_at	A4883074	nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788
206765_at	AF153820.1	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108
213351_s_at	A1934469	KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705
214590_s_at	AL545760	ubiquitin-conjugating enzyme E2D1	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1	<i>leukotriene B4 ornithine hydrolase (CYP4F3)</i>	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773
210992_x_at	U90939.1	Fc gamma receptor IIc2	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239
20528_at	NM_018399.1	VNN3 protein	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216
200919_at	NM_004427.1	early development regulator 2	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056
207387_s_at	NM_000167.1	glycerol kinase	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603
117_at	X51757	heat-shock protein HSP70B	1.1	0.2	0.8	0.6	0.9	0.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139
205174_s_at	NM_012413.2	glutathione S-transferase glut																				

Fig. 6E

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C. Neutrophil (Ne)-selective transcripts (3/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	NeSL
207624_s_at	NM_000328.1	retinoid pigmentosa GTPase	0.0	0.6	1.1	2.0	1.2	1.1	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3
209850_s_at	BC005406.1	regulator (RPCR)	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	0.2	0.2	0.2	0.6	0.4	1.6
209336_s_at	NM_004994.1	Ccr42 effector protein 2	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	35.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3
215966_x_at	AA292874	matrix metalloproteinase 9	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	0.2	0.1	0.2	1.3	0.5	0.0
206925_at	NM_005668.1	glycerol kinase	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	1.4	0.4	0.9	1.6	1.2	0.2
211764_s_at	BC005980.1	sialyltransferase 8	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3
201192_s_at	NM_006224.1	ubiquitin-conjugating enzyme E2D 1	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2
205921_s_at	U16120.1	prophosphatidylinositol transfer protein (PITPN)	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	0.0	0.1	0.3	1.1	0.3	0.4
209137_s_at	BC000263.1	ubiquitin C-terminal hydrolase	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7
208052_x_at	NM_001815.1	related polypeptide	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5
201393_s_at	NM_000876.1	carcinoembryonic antigen-related cell	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	14.8
218614_at	NM_018169.1	adhesion molecule 3 (CEACAM3)	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8
202084_s_at	NM_003003.1	insulin-like growth factor 2 receptor	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7
32069_at	AB014515	FLJ10652	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1
205896_at	NM_003059.1	SEC14 (S. cerevisiae)-like 1	0.8	1.2	1.0	0.1	1.9	2.4	3.5	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5
206884_at	NM_015364.1	KIAA0615	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5
202082_s_at	NM_003003.1	MD-2 protein	1.0	0.3	3.6	2.5	2.2	1.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3
204308_s_at	NM_014844.1	SEC14 (S. cerevisiae)-like 1	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3
207500_at	NM_004347.1	KIAA0329	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1
203435_s_at	NM_007287.7	caspase 5	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2
205539_at	NM_005761.1	CD10, membrane	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7
204601_at	NM_014664.1	metallo-endopeptidase	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9
201963_at	NM_021122.2	adiponin	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5
207064_s_at	NM_009590.1	adiponin	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8
220005_at	NM_023914.1	alpha	0.6	0.0	0.1	0.5	0.1	1.9	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6
211395_x_at	U90940.1	P2YX purinergic receptor GPR86	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	0.0
201780_s_at	NM_007282.1	for UDP-glucose	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2
209864_at	AB045118.1	Fe gamma receptor Ilc3	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5
218319_at	NM_020651.2	ring finger protein 13 (RNF13)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.6
206632_s_at	NM_004900.1	GSK-3 binding protein FRAT2	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0
220950_s_at	NM_030938.1	pellino (Drosophila) homolog 1	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4
221653_x_at	BC004395.1	(PELI1)	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1
204748_at	NM_00963.1	phorbol	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3
210423_s_at	L32185.1	COX2 prostaglandin-endoperoxide	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0
206429_at	NM_005242.2	synthase 2	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3
213352_at	AB954469	integral membrane protein	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3
201888_s_at	U81379.3	PAR2 proteinase activated receptor-2	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.3	2.9	1.3
		KIAA0779																		
		interleukin-13 receptor																		

Fig. 6F

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C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #	Transcripts	MC	cond	MC	Ba2	Ba3	Eo	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	pI	CD4	CD8	CD14	CD19	Fb	Ba.SL
204780_s_at	AA164751	CD95, Fas, APO-1	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
209310_s_at	U25804.1	phosphatidylinositol glycan, class B (PIGB)	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
205452_at	NM_004855.1	FLJ20950	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	1.6	1.6	2.2	3.9	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1	swine acylneuraminase lyase	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	3.7	3.4	3.7	3.9	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1	chromosome 1 open reading frame	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	2.0	2.3	2.3	1.8	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005369.1	12 clone MGC12484	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	2.9	3.2	2.4	2.1	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670	ferritin, light polypeptide-like 1	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1	guanine nucleotide binding protein 10 (GNG10)	7.1	5.4	2.6	6.7	6.5	11.7	11.4	2.0	15.3	4.5	8.7	8.3	5.7	0.8	2.7	3.0	8.4	3.2	1.2	4.5644
209600_s_at	S69189.1	peroxisomal acyl-coenzyme A oxidase	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	1.5	1.7	2.1	2.1	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_002029.1	formyl peptide receptor 1	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	28.2	31.5	27.4	25.2	3.6	1.3	0.7	6.2	1.1	0.5	4.505
217738_at	BF57514	pre-B-cell colony-enhancing factor	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
215078_at	AL050388.1	DKFZp564M2422	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
215418_at	NM_033744.1	numb (Drosophila) homolog	1.1	0.4	0.7	1.5	2.4	2.7	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
218023_s_at	NM_002153.1	heat shock 70kD protein 6 (HSP70B)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	10.5	17.0	10.4	9.6	7.0	7.0	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
210865_s_at	BC001906.1	putative nuclear protein (LOC51307)	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.8	4.3383
207643_s_at	NM_001065.1	Similar to miraxin 1	1.8	1.6	0.9	1.3	1.4	6.3	7.4	8.5	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
203140_at	NM_001706.1	R-cell CLL lymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.2	5.9	17.4	0.6	16.0	4.2796
207253_s_at	NM_016936.1	ubiquitin 1	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.4	6.7	6.5	4.2767
20875_s_at	BE39771.5	pre-B-cell leukemia transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1	FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1	Usurpin-beta	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	36.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1	bromodomain adjacent to zinc finger domain, 1A	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1	nitin	4.1	1.9	6.4	7.4	9.0	24.2	14.8	25.6	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	AB06395	KIA40993	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.8	4.1806
208485_x_at	NM_003879.1	CASP8 and FADD-like apoptosis regulator (FELAR)	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1	gp 180-carboxypeptidase D-like enzyme	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	8.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
220933_s_at	NM_024617.1	FLJ13409	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186	glycerol-3-phosphate dehydrogenase	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	8.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006068.1	Toll-like receptor 6	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1	chromosome 6 open reading frame 76	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1	FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA858754	KIA0050	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1	RIKEN cDNA 5830420C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1	apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985	acyl-Coenzyme A oxidase 1, palmitoyl	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1	sialyltransferase (ST6M)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Fig. 6G

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C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #	Transcripts	MC, cord blood	Ba2 (small)	Ba3 (small)	EO 1 (small)	EO 2 (small)	EO 3 (small)	EO 4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	p CD4	CD8	CD14	CD19	Eb	NeSL
20407_s at	NM_005802.1	tumor protein p53-binding protein	1.4	1.6	1.1	2.9	3.7	2.3	2.6	2.2	10.5	12.8	8.0	11.9	1.5	2.2	1.4	2.2	2.1
210594_x at	AF239756.1	myelin protein zero-like 1	1.2	0.5	0.6	1.2	0.1	0.4	0.8	1.9	1.53	13.9	7.1	10.9	0.3	0.2	0.6	0.7	2.8
203063 at	NM_014634.1	protein phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	29.6	31.8	0.3	2.9	1.2	7.3	1.8
201392_s at	BG031974	insulin-like growth factor 2 receptor	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	12.8	15.0	1.1	1.2	4.0	3.8	7.0
221477_s at	B575213	MG52618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	36.1	46.6	7.9	3.2	1.2	12.6	2.1
206756 at	NM_019886.1	carbohydrate (N-acetylglucosamine 6-O)-sulfoesterase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	10.5	0.1	1.3	1.0	1.0	0.5
204994 at	NM_002463.1	myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	80.8	2.4	7.5	6.0	15.6	1.8
201943_s at	NM_001304.2	carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	15.2	0.7	1.0	1.7	3.3	3.8
216252_x at	Z70519.1	CD95, Fas, APO-1	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	8.4	2.2	3.8	2.4	1.9	3.9
203066 at	NM_014863.1	B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	86.9	1.9	0.1	0.0	19.3	4.2
212479_s at	AL050139.1	FUJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	9.8	1.1	2.3	2.4	2.2	5.9
209571 at	U03644.1	CASP8 and FADD-like apoptosis receptor	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	10.9	0.8	1.0	1.1	1.2	1.1
211317_s at	AF041461.1	regulator C-type (calcium dependent, carbohydrate-recognition domain)	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	17.6	2.4	4.7	6.5	5.7	4.9
209732 at	BC005254.1	lectin, superfamily member 2	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	75.5	4.1	14.4	21.2	10.2	16.4
201779_s at	AF070558.1	clone 24450 RING zinc finger protein RZF	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	81.8	6.0	9.6	11.3	25.7	15.7
212441 at	D86985.2	KIAA0232	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	49.8	2.5	2.0	4.0	5.9	2.1
205920 at	NM_003043.1	solute carrier family 6, member 6 (SLC6A6)	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	4.0	0.3	0.1	0.4	2.6	0.1
213596 at	AL050391.1	DKFZP586A181	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	9.9	2.2	1.1	2.0	1.5	0.7
209508_x at	AF005774.1	caspase-like apoptosis regulatory protein (clarp)	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	40.8	2.7	4.0	5.1	6.3	3.4
218115 at	NM_018154.1	FUJ10604	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	7.7	1.1	1.2	2.2	2.1	1.7
215652 at	AK024382.1	FUJ14320	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	2.5	0.1	0.3	1.0	0.9	0.2
212561 at	AA349395	RAB6 interacting protein 1	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	37.1	4.0	8.7	9.9	13.9	5.9
204166 at	NM_014963.1	KIAA00963	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.2
21874 at	AB03745.1	KIAA1324	0.3	0.3	0.3	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5
217207_s at	AK025267.1	butyrophilin like receptor	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9
212579 at	AA868754	KIAA0650	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	39.7	2.0	5.4	5.7	3.1	10.5
212657_s at	AW083357	IL-1 receptor antagonist IL-1Ra (IL-1RN)	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	35.5	0.6	0.8	0.3	9.3	0.4
202392_s at	NM_014338.1	phosphatidylserine decarboxylase aminase (ARGL)	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	32.3	0.8	1.6	1.4	4.2	1.4
206177_s at	NM_000045.2	LPS-induced TNF-alpha factor (LITAF)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	5.0	1.1	0.1	0.4	0.6	0.7
200706_s at	NM_004862.1	PIG7	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	150.2	8.5	13.3	42.7	14.3	16.7
212478 at	AL050139.1	FUJ13910	0.1	0.1	0.2	0.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	6.5	0.1	0.3	1.1	0.6	0.4
218660 at	NM_003494.1	dystralin	2.5	0.5	1.5	0.2	2.3	1.7	0.2	2.6	1.1	48.5	51.8	20.4	3.3	1.2	1.7	10.6	0.2
211982_x at	AL546600	exportin 6	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	6.6	17.5	17.4	9.6	11.5
202748 at	NM_004120.2	guanylate binding protein 2, interferon-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	24.8	4.2	7.3	9.0	6.3	1.9
220088 at	NM_001736.1	Csa receptor	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	91.1	2.3	1.2	0.5	25.6	1.0
202890 at	T62571	microtubule-associated protein 7	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1
220987_s at	NM_030952.1	DNFZ94341037	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.6	5.3	4.7	4.8	11.1	13.3

Fig. 6H

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C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	NeSL
207072_at	NM_003853.1	interleukin 18 receptor accessory protein (IL18RAP)	5.9	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	3.5722
215719_x_at	X83493.1	CD95, Fas, APO-1	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	3.5657
218404_at	NM_013322.1	sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3.563
219394_at	NM_024419.1	phosphatidylglycerophosphate synthase (PGCST)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	3.5544
216913_s_at	AK071460.1	KIAA0650	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	3.5402
205118_at	M60626.1	formyl peptide receptor 1	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	3.5295
210564_x_at	AF09619.1	FLAME-1-delta	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	3.5148
213607_x_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3.514
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	3.5126
210233_at	AF167343.1	interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	3.5023
204959_at	NM_002432.1	myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	3.4903
217967_s_at	AF288391.1	niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	3.4847
221763_at	A1694023	thyroid hormone receptor-interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	3.4777
207857_at	NM_006866.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	3.4773
220740_s_at	NM_005135.1	solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	3.4722
217739_s_at	NM_005746.1	pie-B-cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242
205041_s_at	NM_006071.1	orosomucoid 1 (ORM1)	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189
214784_x_at	BE566299	exportin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155
217985_s_at	AA102574	bromodomain adjacent to zinc finger domain, 1A	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	3.3999
212598_at	A1806395	KIAA0593	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	3.3933
219053_s_at	NM_017966.1	FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	3.3686
217475_s_at	AC020273	PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	3.3448
46323_at	AL120741	Ca ²⁺ -dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	3.3028
201965_s_at	NM_015046.1	KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	3.3019
203628_at	NM_000875.2	insulin-like growth factor 1 receptor	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	3.3989
202193_at	NM_005569.2	LIM domain kinase 2 (LIMK2)	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	3.2887
203042_at	NM_002294.1	transcript variant 2a	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3.282
203226_s_at	NM_018071.1	lysosomal-associated membrane protein 2 (LAMP2)	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	3.2759
212470_at	AB011088.1	FLJ10357	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	3.2688
211133_x_at	AF09643.1	sperm associated antigen 9	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	3.2526
219313_at	NM_017577.1	clone 6 immunoglobulin-like transcript 5	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	3.2404
221149_at	NM_018485.1	DMP2p434C0328	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	3.2282
203433_at	NM_006441.1	G-protein-coupled receptor GPR77	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	3.2181
214486_x_at	AF041459.1	5,10-methylenetetrahydrofolate synthetase	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	3.2114
		FADD-like apoptosis regulator																				

Fig. 61

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C. Neutrophil (Ne)-selective transcripts (7/77).

MC	cord blood	Transcripts	Accession #	Probe set	MC	lung	Ba 1	Ba 2	Ba 3	Fo 1	Fo 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	BaSL
1.3	0.2	oxysterol binding protein-like 2	BC000296.1	209222_s_at	0.2	2.7	8.8	8.0	5.4	5.4	7.7	7.3	17.2	18.4	22.3	23.9	0.9	2.3	3.4	2.8	2.0	1.3	3.1877	
3.3	3.4	ubiquitin-conjugating enzyme E2B	AA877765	202334_s_at	3.4	4.8	15.5	12.1	5.3	7.2	14.7	12.8	20.9	25.6	43.6	38.1	4.0	4.5	3.9	2.5	4.9	4.6	3.1871	
3.7	2.4	mitogen-activated protein kinase 4	NM_003010.1	203266_s_at	2.4	4.9	8.2	6.3	2.5	4.8	6.8	5.0	14.7	15.2	27.4	26.9	2.8	2.4	2.6	2.7	2.3	2.7	3.1804	
4.5	5.4	FLJ10357	R42449	58780_s_at	5.4	1.5	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	0.2	5.7	3.1803	
3.8	1.9	LIM domain kinase 2	AL117466.1	210582_s_at	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609	
1.3	0.2	ELKS transcription factor-like protein 1	AL080144.1	214766_s_at	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414	
9.8	6.2	TRAF and TNF receptor-associated protein (AD22)	NM_016614.1	202266_at	6.2	9.4	23.7	20.9	8.6	9.9	16.5	14.0	36.1	56.5	64.5	57.5	4.5	7.7	9.4	5.3	8.2	6.3	3.1402	
2.1	2.8	BRAF55/HDAC2 complex (80 kDa) transmembrane	NM_016621.1	203278_s_at	2.8	2.7	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.1	3.0	4.5	3.1	2.7	3.0	3.1382	
0.1	1.2	gamma-carboxyglutamic acid protein 4	NM_024081.1	207291_at	1.2	1.3	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336	
8.5	4.5	Dicer1, Dcr-1 homolog (Drosophila)	BC590131	213229_at	4.5	19.5	12.9	15.4	15.9	9.7	19.1	16.0	35.2	39.0	61.4	69.4	6.2	5.9	7.3	15.2	12.2	5.0	3.1306	
1.7	1.7	solute carrier family 31	NM_001860.1	204204_at	1.7	1.3	0.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	2.0	1.2	1.2	8.9	0.2	0.4	3.1262	
8.3	7.3	ornithine decarboxylase antizyme clone 17.6 Immunoglobulin-like transcript	AF242521.1	201364_s_at	7.3	4.4	2.2	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	2.2	5.1	6.3	12.2	6.2	9.6	3.1253	
1.4	0.1	v-yes-1 Yarnaguchi-sarcoma viral related oncogene homolog (LYN)	AF009634.1	210784_x_at	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236	
6.9	6.9	hypothetical protein MGC26706	AJ356412	202625_at	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	1.7	0.9	17.1	23.6	0.5	3.1131	
2.2	0.5	major histocompatibility complex, class I, B	AW469184	221895_at	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.6	3.11	
2.5	3.0	retinitis pigmentosa GTPase regulator interacting protein 1 (RGRIP1)	D13640	3737384_at	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.6	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985	
1.1	1.4	tol-like receptor 2	NM_020366.1	206608_s_at	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091	
1.8	0.1	CD95, Fas, Apo-1	NM_003264.1	204924_at	0.1	2.1	8.2	7.6	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.1	26.3	0.9	0.4	3.0909	
2.0	2.0	KIAA0993	NM_000043.1	204781_s_at	1.1	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0827	
3.1	2.9	FLAME-1	AJ806395	212606_at	2.0	0.0	0.7	0.6	0.7	0.0	0.1	0.1	18.0	14.3	25.0	26.9	0.1	0.2	0.3	6.6	0.0	3.4	3.0797	
4.4	2.5	ninjurin 1	AF009616.1	211316_x_at	2.9	20.1	19.4	31.9	11.6	11.9	20.6	19.1	58.8	74.1	72.8	81.0	4.1	6.8	8.7	10.3	5.5	2.6	3.0752	
3.0	3.7	intercellular adhesion molecule 3 (ICAM3)	NM_004148.1	203045_at	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746	
0.2	0.6	carbonic anhydrase IV (CA4)	NM_002162.2	204949_at	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	19.9	1.3	3.0617	
2.1	1.7	metallo phosphoesterase	NM_000717.2	206708_at	0.6	0.1	0.1	0.1	1.1	0.7	1.0	0.8	5.6	5.2	2.8	2.4	1.2	0.1	0.1	0.1	0.1	0.1	3.0572	
15.5	9.5	v-yes-1 Yarnaguchi sarcoma viral related oncogene homolog (LYN)	AJ43654	213727_x_at	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554	
1.1	0.3	immunoglobulin superfamily, member 6 (IGSF6)	NM_002350.1	202626_s_at	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442	
21.4	17.4	protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	NM_005849.1	206420_at	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391	
2.0	1.0	zinc finger protein 267	AU150728	219540_at	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361	
6.0	5.4	v-rat-1 thymine leukemia viral oncogene homolog 1 (RAF1)	NM_002880.1	201244_s_at	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.6	7.3	3.0329	
1.4	1.2	mitogen-activated protein kinase 4	AA810268	203265_s_at	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028	
0.0	0.0	RAR receptor-like protein-tyrosine phosphatase	AF007555.1	203030_s_at	0.0	1.6	1.2	0.1	0.1	0.1	0.1	0.1	0.8	3.0	1.1	2.8	0.1	0.1	0.0	0.1	0.0	0.0	3.0269	
1.9	2.6	zinc finger protein 217	NM_006526.1	203739_at	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0158	
2.0	3.0	interferon-induced protein with tetratricopeptide repeats 4 (IFIT4)	NM_001549.1	204747_at	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	6.2	1.4	2.6	3.0143	
0.7	1.0	carbonic anhydrase IV (CA4)	NM_000717.2	206209_s_at	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.1	1.0	0.5	0.9	1.0	0.5	3.0112	

Fig. 6J

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D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	MCSL
217023_x.at	AF099143	tryptase beta	1694	1187	07	11	04	01	01	05	01	02	01	06	04	03	01	01	02	01	02
215382_x.at	AF206666.1	tryptase beta	1881	1084	17	07	04	02	02	02	01	01	03	01	01	02	01	01	01	01	05
204041_at	NM_000898.1	monamine oxidase B	235	469	02	07	01	01	02	06	03	03	01	02	01	02	01	02	01	02	172668
210084_x.at	AF206665.1	tryptase alpha	1311	923	07	12	12	02	01	01	01	01	01	01	01	06	01	00	01	01	112376
216474_x.at	AF206667.1	tryptase beta	2100	1209	24	20	14	12	04	02	01	02	11	01	01	18	08	09	01	01	843375
205683_x.at	NM_003294.2	tryptase beta	1955	953	24	27	03	02	02	06	06	04	01	04	10	20	07	02	03	02	672617
207741_x.at	NM_003293.2	tryptase alpha	1750	997	22	22	18	05	02	03	02	06	02	03	03	22	07	01	05	03	59015
207134_x.at	NM_024164.2	tryptase beta	2146	1123	31	38	17	12	03	08	06	03	08	04	01	05	02	01	11	03	571834
205653_at	NM_001911.1	cathepsin G	912	570	27	11	09	09	04	31	08	03	14	16	06	07	02	04	13	03	514769
205266_at	NM_003092	leukemia inhibitory factor	170	98	02	02	03	03	01	02	02	01	02	04	07	01	02	01	01	01	443659
210324_at	M17263.1	complement protein C5 gamma	29	69	01	01	00	00	00	01	01	03	01	01	01	01	01	00	00	01	33806
211743_s.at	BC005929.1	major basic protein	743	707	10	47	27	01	07	08	06	02	03	07	02	01	02	02	03	02	315959
211549_s.at	U63296.1	15-hydroxyprostaglandin dehydrogenase	483	483	21	25	14	15	13	08	09	01	01	02	01	11	05	08	05	05	248454
206726_at	NM_014485.1	prostaglandin D2 synthase	1190	940	50	78	57	07	01	10	05	02	02	02	06	13	07	03	12	03	17452
205011_at	NM_014622.1	loss of heterozygosity, 11,	761	709	30	68	45	23	10	14	19	02	11	12	18	29	22	13	17	20	162511
205428_s.at	NM_001740.2	chromosomal region 2, gene A	167	634	13	07	09	04	16	07	13	18	16	36	15	17	07	11	13	06	161621
219255_at	NM_024554.1	calbindin 2 FLJ11413	100	92	01	01	01	02	01	06	06	01	06	01	02	01	06	01	06	00	15639
204468_s.at	NM_005424.1	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	36	28	05	03	01	00	01	02	00	00	00	01	01	00	00	00	01	00	144259
208343_s.at	AF146343.1	CYP7A promoter binding factor	15	09	00	00	03	01	00	01	00	01	00	02	04	01	00	00	00	00	138025
205051_s.at	NM_000222.1	CD117 c-KIT	921	858	62	81	73	23	52	65	27	07	21	08	11	08	02	05	01	01	123815
210102_at	BC001234.1	loss of heterozygosity, 11,	409	411	28	37	45	03	04	03	06	07	09	02	06	18	08	07	12	06	113619
210796_x.at	D86359.1	chromosomal region 2, gene A	178	260	15	10	11	12	15	13	14	14	23	17	13	20	14	15	18	10	105398
206519_x.at	D86358.1	static acid binding Ig-like lectin, siglec6	34	79	00	03	04	00	00	00	01	00	01	05	02	05	00	00	00	04	1013
206480_at	NM_000897.1	leukotiene C4 synthase	88	160	03	02	06	24	16	05	01	02	11	01	01	13	01	03	01	01	927381
206617_s.at	NM_002910.4	renin-binding protein	106	62	12	01	04	28	16	05	01	06	21	01	01	09	02	07	03	04	918529
208089_s.at	NM_030794.1	tudor domain containing 3	60	134	08	06	02	05	07	05	05	01	06	03	00	07	07	11	08	06	816897
205466_s.at	NM_005114.1	heparan sulfate 3-O-sulfotransferase ADAMTS3 a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	181	72	01	04	01	07	01	03	02	04	01	08	04	01	00	00	02	14	815381
214913_at	AB002364.1	tissue-plasminogen activator	68	43	05	07	08	05	07	06	04	05	04	07	12	07	06	05	04	05	72214
201860_s.at	NM_000930.1	static acid binding Ig-like lectin, siglec6	222	297	02	04	01	01	03	05	05	01	01	13	04	16	01	02	06	01	36
206520_x.at	NM_001245.1	L88 protein	190	227	24	11	08	11	15	13	10	20	20	04	14	29	21	23	19	19	710132
220532_s.at	NM_014020.1	FLJ10305	524	182	08	08	10	64	29	15	12	04	05	14	06	22	06	02	50	01	61662
218169_at	NM_018052.1	nuclear receptor subfamily 1, group I, member 3	62	146	03	02	04	04	03	03	04	06	05	01	01	05	02	14	16	03	604597
221728_x.at	AK025198.1	tudor domain containing 3	56	55	06	09	10	04	36	09	08	07	06	14	09	09	08	07	07	08	570228
214028_x.at	AU156998	lipase	32	119	09	00	04	08	03	04	07	06	06	01	01	08	12	11	01	07	510738
221552_at	BC001698.1	MKP-1 like protein tyrosine phosphatase (MKP-1)	106	34	09	18	11	09	11	10	09	02	02	07	01	01	02	07	09	03	502434
203367_at	NM_007026.1	heparan sulfate 6-O-sulfotransferase	150	454	12	09	08	09	09	08	01	02	07	04	20	09	10	27	05	14	500514
206997_s.at	NM_004807.1		42	38	02	01	01	04	04	01	03	03	04	03	07	03	02	06	03	08	48127

Fig. 6K

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D. Mast cell (MC)-selective transcripts (2/2).

Probe set		Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	EO 1 (small)	EO 2 (small)	EO 3 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	p1 CD4	CD8	CD14	CD19	Fb	MCSL		
207480_s_at	45288_at	NM_020149.1 AA209239	TAL1 homeobox protein Meis2e lipase	140 109	149 3.0	1.9 0.2	3.6 2.1	4.0 0.8	1.7 0.5	1.9 0.5	5.3 1.3	3.8 0.9	0.3 0.1	0.6 0.1	1.0 0.2	0.3 0.1	0.5 0.4	0.8 0.5	0.4 1.3	0.8 1.0	0.9 0.9	4.72642 4.52869	
207039_at	201650_at	NM_000077.1 NM_002276.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) keratin 19	75 62	3.6 12.0	0.7 0.0	0.7 0.0	0.1 0.3	0.6 0.1	0.4 0.0	0.3 0.0	0.5 0.1	1.2 0.1	0.6 0.1	0.6 0.1	1.1 0.1	0.1 0.0	0.9 0.1	0.5 0.1	0.8 0.1	0.1 0.0	1.2 2.0	4.35629 4.35547
214533_at		NM_001836.1	chymase	101	2.7	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3	4.27984
218211_s_at	203916_at	NM_024101.1 NM_003635.1	melanophilin N-deacetylaseN-sulfotransferase	248 179	29.6 26.7	2.7 3.2	2.5 6.5	1.8 6.8	3.0 2.5	2.5 2.7	1.9 3.6	2.2 3.1	4.6 4.2	4.1 3.4	3.3 5.5	4.1 5.2	6.4 0.9	4.0 3.1	3.2 4.9	2.4 3.3	2.7 2.4	4.24499 4.20693	
212336_at	200766_at	AB002336.1 NM_001909.1	erythrocyte membrane protein band 4.1-like 1 cathepsin D	38 426	6.4 39.5	0.1 2.5	0.2 5.3	0.1 4.3	0.5 4.3	0.1 4.8	0.2 3.4	0.4 2.7	0.1 4.0	0.1 6.7	0.1 3.1	0.5 1.9	0.1 2.6	0.4 1.6	0.2 2.5	0.4 10.0	0.4 1.6	1.2 5.9	4.12758 4.1037
202218_s_at	204066_s_at	NM_004265.1 NM_014914.1	delta-6 fatty acid desaturase (FADS6) centaurin, gamma 2	188 53	24.5 7.9	0.4 0.4	0.2 0.4	1.0 0.7	0.3 0.2	0.1 0.2	0.8 0.6	0.5 0.6	0.2 0.3	0.1 0.5	0.1 0.4	0.1 0.4	1.6 0.8	0.1 0.6	0.6 1.6	0.1 0.6	0.5 1.0	4.08548 4.06712	
209644_x_at	221679_s_at	U38945.1 AF225418.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) lipase	140 28	6.4 1.9	1.0 0.4	1.4 0.9	0.7 0.1	1.2 0.3	1.3 0.4	1.7 0.4	1.5 0.1	1.0 0.1	1.6 0.5	1.5 0.0	2.1 0.5	2.3 0.5	1.8 0.1	1.5 0.6	0.9 0.5	0.3 0.2	2.4 3.88459	
211538_s_at	211548_s_at	U56725.1 J05594.1	heat shock protein 70kD 15-hydroxyprostaglandin dehydrogenase	4.4 82.6	7.4 60.0	0.3 19.4	0.6 26.0	0.4 16.3	0.6 3.2	0.3 2.9	0.3 1.8	0.9 1.7	1.4 0.8	0.4 0.5	1.0 0.9	0.8 0.2	1.5 4.1	0.5 1.2	0.5 0.9	0.1 0.1	0.5 0.6	0.7 3.49258	
210174_at	219412_at	AF228413.1 NM_022337.1	member 2 RAB38, member RAS oncogene	2.9 3.9	3.4 4.0	0.5 0.1	0.5 0.4	0.6 0.3	0.8 0.7	1.1 0.1	0.7 0.2	1.2 0.3	1.1 0.2	0.4 0.2	0.1 1.1	0.4 1.2	0.7 0.1	0.2 0.8	0.2 0.4	0.6 0.1	0.3 0.5	3.47124 3.32805	
201850_at	205888_s_at	NM_001747.1 A1962693	gelosin-like capping protein (actin filament) KIAA0555	70.5 5.4	64.5 4.6	9.6 0.7	30.8 1.6	28.8 1.2	8.1 0.8	7.8 0.7	11.5 0.1	9.9 1.0	2.6 1.3	3.6 0.3	3.0 0.2	2.4 0.6	1.6 1.2	1.1 0.3	1.0 1.5	1.0 0.7	5.8 1.2	5.3 0.4	3.29919 3.25197
221750_at		BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1926
214218_s_at	218788_s_at	AV699347 NM_022743.1	nuclear receptor subfamily 1, group 1, member 3 FLJ21080	3.5 16.1	3.5 23.7	0.7 0.5	0.6 2.3	0.7 2.5	0.5 0.9	2.2 1.1	0.5 2.7	0.7 2.1	1.2 1.1	1.2 1.0	0.6 0.8	1.1 0.9	0.9 2.3	0.3 2.1	0.6 2.9	0.6 0.6	0.8 2.0	0.4 6.3	3.15254 3.07851
218087_s_at	2221577_x_at	NM_015385.1 AF003934.1	SH3-domain protein 5 (ponsin) prostate differentiation factor	1.4 7.8	1.9 5.5	0.4 0.6	0.9 0.3	0.4 0.5	0.5 0.6	0.0 0.1	0.0 0.2	0.0 0.3	0.0 0.2	0.1 0.3	0.1 0.3	0.2 0.3	0.1 0.2	0.0 0.0	0.2 0.1	0.2 0.1	0.2 0.4	0.1 2.1	3.07366 3.05532
35820_at	208744_x_at	X62078 BG403660	GIM2 activator protein heat shock 105kD	21.8 7.3	17.6 4.8	1.4 0.5	3.3 0.2	1.3 0.2	0.3 0.9	0.3 0.1	0.2 0.4	0.5 0.6	0.8 0.1	0.1 0.1	1.9 0.3	0.4 0.8	0.2 1.7	0.2 2.0	0.2 0.9	0.2 0.9	6.5 0.9	5.0 2.0	2.7 3.00671

Fig. 6L

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E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cond	MC blood	Ba.1 (small)	Ba.2 (small)	Ba.3 (small)	Eo (small)	Eo (small)	Eo3 (small)	Eo4 (small)	Ne (small)	Ne (small)	Ne3 (small)	Ne4 (small)	CD4	CD8	CD14	CD19	Fb	Ba/Eo SL		
R	M6651.1 M75914.1	IL-3R interleukin 5 receptor alpha IL-3R interleukin 5 receptor alpha CRTH2 chemotactant	0.6 0.2	1.6 1.6	11.8 15.4	28.2 30.8	17.9 15.3	16.4 18.7	25.3 40.2	32.6 29.7	29.5 33.0	0.0 0.3	0.7 0.2	0.0 1.5	1.0 0.5	0.0 0.1	0.4 0.1	0.2 0.1	0.0 0.1	0.2 0.1	0.0 0.1	61.956 42.811	
GPR	NM_004778.1 NM_001828.3 NM_022969.1	receptor-homologous molecule expressed on Th2 cells Charcot-Leyden crystal protein fibroblast growth factor R2 egf-like module containing mucin-like, hormone receptor-like sequence 1 (EMR-1)	1.8 1.1 0.2	0.3 0.1 0.1	22.0 27.0 7.3	40.5 219.1 43.5	15.3 203.6 330.4	33.7 226.8 4.1	37.9 233.8 8.8	38.9 179.7 12.3	42.3 163.1 23.3	1.0 2.1 0.1	2.6 19.4 0.1	2.2 19.1 0.3	2.1 49.3 0.3	0.8 2.8 0.1	1.4 1.0 0.1	1.0 1.4 0.2	1.2 0.9 0.1	0.9 0.7 0.1	0.5 0.4 1.0	16.642 15.164 13.357	
GPR	NM_001974.1 AU145003	FLJ1581 fts clone HEMBA 1003598 dachshund (Drosophila) homolog Hs63931	1.5 0.7	0.1 0.3	16.4 5.7	49.5 4.7	34.5 5.2	85.9 4.5	93.1 2.1	91.2 2.8	93.5 2.1	2.7 1.0	3.7 0.1	3.7 0.1	5.4 0.1	3.4 0.2	1.7 0.1	0.8 0.1	7.1 0.1	1.6 0.1	0.5 0.2	8.092 7.2618	
	AW772082 NM_025080.1 NM_021624.1 NM_01769.1 NM_014666.1	FLJ22316 histamine receptor H4 entrophoxin secreted fibroblast growth factor receptor (K-sam, III)	0.1 0.2 0.2 7.8	0.6 0.5 0.5 9.1	5.1 18.0 4.5 41.7	4.1 35.3 12.5 101.5	3.7 18.6 8.9 78.0	6.4 13.7 1.9 26.8	8.3 12.5 2.6 34.1	9.0 16.3 4.2 40.5	7.6 15.4 2.9 35.7	0.8 1.3 0.5 3.0	0.9 1.7 0.6 2.9	1.0 0.9 1.1 3.6	0.8 0.3 0.6 4.5	0.1 0.5 0.4 1.3	0.3 0.4 0.7 6.9	0.5 0.4 0.5 8.0	0.7 0.2 0.0 9.0	0.3 0.3 0.0 7.9	6.8198 6.5045 5.9783 5.1015		
R	M87771.1 AL049987.1 NM_001928.1 AU57637	CD244 natural killer cell receptor 2B4 calcium channel, voltage-dependent, L type, alpha 1D subunit	0.3 0.8 3.5	1.4 0.0 0.1	3.7 10.8 62.0	10.2 46.8 206.0	8.3 44.7 176.5	3.9 6.7 62.4	8.9 6.1 48.1	8.9 6.1 48.1	4.5 25.8 60.5	8.3 20.6 44.8	0.8 1.3 7.1	1.4 4.5 32.5	1.1 4.5 20.5	1.1 4.2 16.3	0.4 2.9 0.1	0.4 1.1 0.6	0.7 2.1 0.1	0.3 3.7 15.6	0.2 2.0 13.6	1.1 0.3 0.8	4.9922 4.7426 4.7202 4.7183
ICN	NM_016382.1 BE550599 M24779.1	protein kinase-related oncogene (pim1) inositol	0.5 0.2 6.8	0.1 0.1 7.1	15.7 1.0 61.3	87.0 1.7 110.3	65.4 2.4 100.1	9.9 0.9 47.0	10.8 0.8 79.7	26.6 2.4 91.6	18.5 1.8 79.5	0.3 0.0 19.2	0.4 0.6 18.8	1.2 0.5 21.1	3.0 0.5 16.1	0.1 0.3 4.1	0.4 0.3 12.7	3.5 0.1 13.9	5.2 0.0 4.6	1.1 0.3 4.0	0.1 0.0 1.2	4.6297 4.5958 4.1983	
GPR	NM_002194.2 NM_001837.1 NM_002934.1 A1970898	polyphosphate-1-phosphatase (pdp1) CR3 chemokine (C-C motif) receptor 3 eosinophil-derived neurotoxin hypothetical protein LOC283445 inositol	5.7 0.2 2.2 0.8	6.2 1.1 2.0 0.7	7.1 107.2 33.7 2.1	25.8 142.9 71.4 4.8	20.5 102.2 38.4 4.3	17.9 46.4 104.7 5.1	24.8 91.7 80.8 4.6	53.6 118.1 47.7 8.0	57.8 107.5 45.1 6.4	2.8 28.3 2.0 1.0	2.7 20.0 2.3 0.8	2.6 26.3 3.1 0.7	4.0 25.1 2.8 0.8	1.9 0.2 1.4 1.1	1.8 0.5 0.7 1.0	2.6 0.4 1.3 0.6	4.8 0.2 1.4 1.1	1.9 0.2 0.7 1.1	4.1158 3.9525 3.7641 3.7554		
GPR	A1039084 U62027.1	polyphosphate-5-phosphatase, 75kD Gsa receptor	0.6 12.4	1.2 11.2	4.3 44.1	8.0 72.3	68.8 50.5	5.6 18.8	38.8	6.3 70.3	9.7 29.9	0.7 1.2	0.5 1.2	2.2 1.8	1.7 3.8	1.4 1.6	1.2 1.5	1.4 3.0	1.0 0.6	1.9 0.5	1.3 0.1	3.6088 3.6039	
	A1539710 AF195624.1 NM_003104.1 BC003629.1 FLJ23438 fts clone HRC13275 NM_018276.1 NM_014867.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 cholesterol phosphotransferase 1 beta sorbitol dehydrogenase (SDH) FLJ10928 FLJ19919 fts clone HRC13275 KIAA0711	8.5 7.0 2.0 1.1 1.1 0.1 0.6	7.0 6.8 1.5 0.1 0.2 0.1	24.2 31.6 2.9 8.3 3.1 3.8	56.2 79.7 4.2 11.0 1.8 14.3	48.9 55.8 4.1 13.3 2.5 10.7	14.2 26.9 7.4 2.4 1.7 5.3	20.0 32.6 11.6 5.1 4.3 6.8	30.1 43.8 8.3 5.1 1.7 12.6	20.7 41.8 11.2 11.1 2.1 10.5	3.0 5.2 1.7 2.5 0.1 0.6	3.6 7.5 2.5 0.5 0.5 0.6	4.3 5.9 1.5 0.2 0.4 1.6	6.0 9.6 1.3 0.7 0.3 1.6	3.8 2.4 7.3 0.3 0.1 1.0	3.5 3.1 1.4 0.2 0.2 0.8	5.4 3.3 1.8 1.2 0.6 1.2	5.1 7.7 1.8 1.2 0.8 2.6	5.5 11.8 1.1 1.8 1.9 0.1	5.3 5.7 1.1 0.5 0.7 0.1	3.5673 3.5626 3.5098 3.2532 3.2497 3.2398	
	U66065.1	Grb 10- and Grb-IR-related splice variant 1	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	0.4	1.6	3.1044	
	D25304.1 L12387.1	RacGdc42 guanine exchange factor (GEF6) sorcyn (SR)	13.1 19.2	24.8 11.4	28.8 20.2	74.7 88.6	73.0 67.0	53.8 37.4	35.5 42.4	92.9 86.3	59.6 85.4	9.2 6.9	6.1 8.9	18.5 17.6	13.7 21.5	3.1 2.6	10.8 11.1	12.9 12.7	7.1 8.4	7.8 8.6	1.0 17.8	3.0943 3.0628	
	AF033026.1	biofunctional ATP sulfonylaseadenosine 5-phosphosulfate kinase	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0	22.7	3.0385	

Fig. 6M

E. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC	32/36																		
				Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2 (small)	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2 (small)	Ne3 (small)	Ne4 (small)	p1	CD4	CD8	CD14	CD19	Fb	Eo+Ne.S.I.	
221345_at	NM_005306.1	GPR43 PAR1-like	0.1	0.4	0.9	0.6	0.6	7.0	166	154	10.5	49.7	45.7	22.5	230	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720	zinc finger, DHHC domain containing 18	2.2	0.8	4.1	3.9	40	160	174	148	16.7	59.2	53.9	30.9	398	1.1	2.4	3.8	2.6	1.5	1.3	65842
211576_s_at	BC003068.1	solute carrier family 19 member 1	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025	nephroblastoma overexpressed gene	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
		ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3																				
218950_at	NM_022481.1		1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	BC12-related protein A1	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1	granulysin	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
		cDNA FLJ36416 f15, clone																				
213241_at	AF035307.1	THYMU2011053	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	hypothetical protein PRO2831	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
		homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2																				
214153_at	BE467941	KIAA0599	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160	Eg4, endothelial differentiation lysophosphatidic acid	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
		G-protein-coupled receptor, 4																				
206723_s_at	AF011466.1	adenosine monophosphate deaminase 2 (isoform L)	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	transforming, acidic coiled-coil containing protein 3 (TACC3)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1	protein kinase C-like 2	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1	serum glucocorticoid regulated kinase (SGK)	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	ectonucleoside triphosphate diphosphohydrolase 1	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV171590	growth arrest and DNA damage inducible protein beta (GADD45B)	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1	iduronate 2-sulfatase	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1		0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

Fig. 6N

G.Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC																				Ba+Ne SL
			cord blood	lung	MC	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD 4	CD 8	CD 14	CD 19	Fb	
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398	
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025	
219157_at	NM_007246.1	kelch (Drosophila)-like 2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523	
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355	
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664	
222151_s_at	AK023738.1	FLJ13676 fs	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372	
207907_at	NM_003807.1	tumor necrosis factor (ligand)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177	
202530_at	NM_001315.1	superfamily member 14 (TNFSF 14)	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469	
217521_at	N54942	mitogen-activated protein kinase 14	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207	
203693_s_at	NM_001949.2	Hs.276590 ESTs	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116	
203420_at	NM_016255.1	E2F transcription factor 3	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188	
218308_at	NM_006342.1	autosomal highly conserved protein (AHCP)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769	
203080_s_at	NM_013450.1	transforming acidic coiled-coil containing protein 3	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401	
219999_at	NM_018621.1	bromodomain adjacent to zinc finger domain, 28	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991	
213805_at	AK692428	hypothetical protein PRO2198	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317	
204669_s_at	NM_007219.2	clone 23551 mRNA	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834	
215555_at	AK023774.1	ring finger protein 24	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591	
		FLJ13712 fs																					

33/36

Fig. 60

34/36

H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1 (small)	Eo 2 (small)	Eo 3 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC+Ba SL
205624_at	NM_001870.1	Carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.5	0.5	59.1989
208605_s_at	NM_002529.2	R	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1	TRK neurotrophin receptor regulator of G protein signaling (RGS13)	6.2	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	21.7762
207496_at	NM_000139.1	R	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	21.1783
203857_at	AI269290	solute carrier family 18	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	20.3301
210358_x_at	BC002557.1	GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	9.46893
207497_s_at	D10583.1	Fc epsilon R1 beta	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	9.39967
203914_x_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGh)	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	6.14285
219557_s_at	NM_020645.1	chromosome 11 open reading frame 14	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	3.38029
204061_at	NM_005044.1	protein kinase, X-linked	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	3.26062
202068_s_at	NM_000527.2	R	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	3.1679
		low density lipoprotein receptor																			

Fig. 6P

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I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC cord blood	MC		Ba 1		Ba 2		Ba 3		Eo		Eo 3		Eo 4		Ne		Ne 3		Ne 4		CD 4		CD 8		CD 14		CD 19		Fb	
				lung		(small)	(small)	(small)	(small)	1	2	(small)	(small)	1	2	(small)	(small)	pl															
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4
205758_at	AW006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	0.5	4.2	3.0	76.1	0.8	0.6	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4
211644_x_at	L14458.1	IgGV-J region	0.2	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1
201743_at	NM_000591.1	CD14	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9
203104_at	NM_005211.1	v-fms M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.1
204627_s_at	M35999.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.2	0.5	0.1	0.0
216442_x_at	AK026737.1	fibronectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	0.2	0.1	92.6	0.1	0.0	0.1	0.2	0.1	0.2	0.1	0.2	0.1	92.6

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

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Probe set	Accession #	Transcripts	MC	Ba 1	Ba 2	Ba 3	EO	EO	EO 3	EO 4	Ne	Ne	Ne 3	Ne 4	pl	CD 4	CD 8	CD 14	CD 19	Fd
AFHX-HSAC07/X00351_3_at	X00351	Transcripts	cord																	
AFHX-HSAC07/X00351_M_at	X00351	beta-actin	blood	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	17569	18295	18782	20805	20661	17542	20399
AFHX-HSAC07/X00351_5_at	X00351	beta-actin		22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22294	19087
AFHX-HUMGAPDH/M33197_3_at	M33197	beta-actin		15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583
AFHX-HUMGAPDH/M33197_M_at	M33197	GAPDH		14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	5929	6429	6098	9756	5180
AFHX-HUMGAPDH/M33197_5_at	M33197	GAPDH		15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464
AFHX-HUMGAPDH/M33197_5_at	M33197	GAPDH		16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1355	4655	6826	6260	9905	5636
The median value of 22283 transcripts				121	1693	853	1122	1109	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	152.5	121.3	107.1	114.1
																				183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Fig. 6R